

C. Kaufman

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/339,153

DATE: 09/02/1999
TIME: 10:46:17

INPUT SET: S33165.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Lok, Si
6 Adams, Robyn L.
7 Jelmsberg, Anna C.
8 Whitmore, Theodore E.
9 Farrah, Theresa M.
10
11 (ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11
12
13
14 (iii) NUMBER OF SEQUENCES: 6
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Zymogenetics
18 (B) STREET: 1201 Eastlake Ave East
19 (C) CITY: Seattle
20 (D) STATE: WA
21 (E) COUNTRY: USA
22 (F) ZIP: 98102
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Diskette
26 (B) COMPUTER: IBM Compatible
27 (C) OPERATING SYSTEM: DOS
28 (D) SOFTWARE: FastSEQ for Windows Version 2.0
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER: 09/339,153
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/906,713
37 (B) FILING DATE:
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Lunn, Paul G
41 (B) REGISTRATION NUMBER: 32,743
42 (C) REFERENCE/DOCKET NUMBER: 97-52
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 206-442-6627
46 (B) TELEFAX: 206-442-6678

ENTERED

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47 (C) TELEX:

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 2831 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

57

58 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

60

61 (A) NAME/KEY: Coding Sequence

62 (B) LOCATION: 34...1755

63 (D) OTHER INFORMATION:

64

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

66

67 TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC 54

68 Met Arg Thr Leu Leu Thr Ile

69 1 5

70

71 TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT 102

72 Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

73 10 15 20

74

75 CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG 150

76 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

77 25 30 35

78

79 ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC 198

80 Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

81 40 45 50 55

82

83 GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT 246

84 Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys

85 60 65 70

86

87 CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC 294

88 Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn

89 75 80 85

90

91 CTC ACG GAG CTC TAC TAT GCC AGG GTC ACC GCT GTC AGT GCG GGA GGC 342

92 Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly

93 90 95 100

94

95 CGG TCA GCC ACC AAG ATG ACT GAC AGG TTC AGC TCT CTG CAG CAC ACT 390

96 Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr

97 105 110 115

98

99 ACC CTC AAG CCA CCT GAT GTG ACC TGT ATC TCC AAA GTG AGA TCG ATT 438

RAW SEQUENCE LISTING PATENT APPLICATION *US/09/339,153*

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100	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
101	120					125					130					135	
102																	
103	CAG	ATG	ATT	GTT	CAT	CCT	ACC	CCC	ACG	CCA	ATC	CGT	GCA	GGC	GAT	GGC	486
104	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
105					140					145					150		
106																	
107	CAC	CGG	CTA	ACC	CTG	GAA	GAC	ATC	TTC	CAT	GAC	CTG	TTC	TAC	CAC	TTA	534
108	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
109				155					160					165			
110																	
111	GAG	CTC	CAG	GTC	AAC	CGC	ACC	TAC	CAA	ATG	CAC	CTT	GGA	GGG	AAG	CAG	582
112	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
113			170					175					180				
114																	
115	AGA	GAA	TAT	GAG	TTC	TTC	GGC	CTG	ACC	CCT	GAC	ACA	GAG	TTC	CTT	GGC	630
116	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
117		185					190					195					
118																	
119	ACC	ATC	ATG	ATT	TGC	GTT	CCC	ACC	TGG	GCC	AAG	GAG	AGT	GCC	CCC	TAC	678
120	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
121	200					205					210					215	
122																	
123	ATG	TGC	CGA	GTG	AAG	ACA	CTG	CCA	GAC	CGG	ACA	TGG	ACC	TAC	TCC	TTC	726
124	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
125				220						225					230		
126																	
127	TCC	GGA	GCC	TTC	CTG	TTC	TCC	ATG	GGC	TTC	CTC	GTC	GCA	GTA	CTC	TGC	774
128	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
129				235					240					245			
130																	
131																	
132	TAC	CTG	AGC	TAC	AGA	TAT	GTC	ACC	AAG	CCG	CCT	GCA	CCT	CCC	AAC	TCC	822
133	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
134			250					255					260				
135																	
136	CTG	AAC	GTC	CAG	CGA	GTC	CTG	ACT	TTC	CAG	CCG	CTG	CGC	TTC	ATC	CAG	870
137	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
138		265					270					275					
139																	
140	GAG	CAC	GTC	CTG	ATC	CCT	GTC	TTT	GAC	CTC	AGC	GGC	CCC	AGC	AGT	CTG	918
141	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
142	280					285					290					295	
143																	
144	GCC	CAG	CCT	GTC	CAG	TAC	TCC	CAG	ATC	AGG	GTG	TCT	GGA	CCC	AGG	GAG	966
145	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	
146				300						305					310		
147																	
148	CCC	GCA	GGA	GCT	CCA	CAG	CGG	CAT	AGC	CTG	TCC	GAG	ATC	ACC	TAC	TTA	1014
149	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	
150				315					320					325			
151																	
152	GGG	CAG	CCA	GAC	ATC	TCC	ATC	CTC	CAG	CCC	TCC	AAC	GTG	CCA	CCT	CCC	1062

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153	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	
154			330					335					340				
155																	
156	CAG	ATC	CTC	TCC	CCA	CTG	TCC	TAT	GCC	CCA	AAC	GCT	GCC	CCT	GAG	GTC	1110
157	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	
158		345					350				355						
159																	
160	GGG	CCC	CCA	TCC	TAT	GCA	CCT	CAG	GTG	ACC	CCC	GAA	GCT	CAA	TTC	CCA	1158
161	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro	
162	360					365				370						375	
163																	
164	TTC	TAC	GCC	CCA	CAG	GCC	ATC	TCT	AAG	GTC	CAG	CCT	TCC	TCC	TAT	GCC	1206
165	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala	
166					380				385						390		
167																	
168	CCT	CAA	GCC	ACT	CCG	GAC	AGC	TGG	CCT	CCC	TCC	TAT	GGG	GTA	TGC	ATG	1254
169	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	Cys	Met	
170				395				400					405				
171																	
172	GAA	GGT	TCT	GGC	AAA	GAC	TCC	CCC	ACT	GGG	ACA	CTT	TCT	AGT	CCT	AAA	1302
173	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys	
174			410				415					420					
175																	
176																	
177	CAC	CTT	AGG	CCT	AAA	GGT	CAG	CTT	CAG	AAA	GAG	CCA	CCA	GCT	GGA	AGC	1350
178	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser	
179		425				430					435						
180																	
181	TGC	ATG	TTA	GGT	GGC	CTT	TCT	CTG	CAG	GAG	GTG	ACC	TCC	TTG	GCT	ATG	1398
182	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met	
183	440				445					450						455	
184																	
185	GAG	GAA	TCC	CAA	GAA	GCA	AAA	TCA	TTG	CAC	CAG	CCC	CTG	GGG	ATT	TGC	1446
186	Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	Gln	Pro	Leu	Gly	Ile	Cys	
187				460			465								470		
188																	
189	ACA	GAC	AGA	ACA	TCT	GAC	CCA	AAT	GTG	CTA	CAC	AGT	GGG	GAG	GAA	GGG	1494
190	Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	Leu	His	Ser	Gly	Glu	Glu	Gly	
191				475			480						485				
192																	
193	ACA	CCA	CAG	TAC	CTA	AAG	GGC	CAG	CTC	CCC	CTC	CTC	TCC	TCA	GTC	CAG	1542
194	Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	Leu	Pro	Leu	Leu	Ser	Ser	Val	Gln	
195			490				495					500					
196																	
197	ATC	GAG	GGC	CAC	CCC	ATG	TCC	CTC	CCT	TTG	CAA	CCT	CCT	TCC	GGT	CCA	1590
198	Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro	
199		505				510					515						
200																	
201	TGT	TCC	CCC	TCG	GAC	CAA	GGT	CCA	AGT	CCC	TGG	GGC	CTG	CTG	GAG	TCC	1638
202	Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser	
203	520				525					530						535	
204																	
205	CTT	GTG	TGT	CCC	AAG	GAT	GAA	GCC	AAG	AGC	CCA	GCC	CCT	GAG	ACC	TCA	1686

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206   Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
207               540                      545                      550
208
209   GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC      1734
210   Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
211               555                      560                      565
212
213   CTG ACT GTG CAG TGG GAG TCC TGAGGGGAAT GGGAAAGGCT TGGTGCTTCC TCCC      1789
214   Leu Thr Val Gln Trp Glu Ser
215               570
216
217   TGTCCCTACC CAGTGTACACA TCCTTGGCTG TCAATCCCAT GCCTGCCCAT GCCACACACT      1849
218   CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGGC ATGCAGGGGCC      1909
219   CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA      1969
220   GCTCTGGGGA GCAGCTTGTG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT      2029
221   GACAGTGCAA GGAGGAAATG CAGGGAAACT CCGGAGGTCC AGAGCCCCAC CTCCTAACAC      2089
222   CATGGATTCA AAGTGCTCAG GGAATTTGCC TCTCCTTGCC CCATTCTGG CCAGTTTCAC      2149
223   AATCTAGCTC GACAGAGCAT GAGGCCCTG CCTCTTCTGT CATTGTTCAA AGGTGGGAAG      2209
224   AGAGCCTGGA AAAGAACCAG GCCTGGAAAA GAACCAGAAG GAGGCTGGGC AGAACCAGAA      2269
225   CAACCTGCAC TTCTGCCAAG GCCAGGGCCA GCAGGACGGC AGGACTCTAG GGAGGGGTGT      2329
226   GGCCTGCAGC TCATTCCAG CCAGGGCAAC TGCCTGACGT TGCACGATTT CAGCTTCATT      2389
227   CCTCTGATAG AACAAAGCGA AATGCAGGTC CACCAGGGAG GGAGACACAC AAGCCTTTTC      2449
228   TGCAGGCAGG AGTTTCAGAC CCTATCCTGA GAATGGGGTT TGAAAGGAAG GTGAGGGCTG      2509
229   TGGCCCTTGG ACGGGTACAA TAACACACTG TACTGATGTC ACAACTTTGC AAGCTCTGCC      2569
230   TTGGGTTCAG CCCATCTGGG CTCAAATTCC AGCCTCACCA CTCACAAGCT GTGTGACTTC      2629
231   AAACAAATGA AATCAGTGCC CAGAACCCTG GTTTCCTCAT CTGTAATGTG GGGATCATAA      2689
232   CACCTACCTC ATGGAGTTGT GGTGAAGATG AAATGAAGTC ATGTCTTTAA AGTGCTTAAT      2749
233   AGTGCCTGGT ACATGGGCAG TGCCCAATAA ACGGTAGCTA TTTAAAAAAA AAAAAAAAAA      2809
234   AAAAAAATAG CGGCCGCCTC GA
235

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

249   Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
250       1           5           10           15
251   Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
252           20           25           30
253   Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
254           35           40           45
255   Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
256       50           55           60
257   Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
258       65           70           75           80

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
11	(ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR	(ii) TITLE OF INVENTION: MAMMALIAN ZCYTOR11
365	(iv) ANTISENSE: YES	(iv) ANTI-SENSE: YES